

Identification of Genes Essential to Long-Chain Alkene Biosynthesis in Micrococcus luteus

Ee-Been Goh, **Jay D. Keasling**, Harry R. Beller*
Presenting author: *Harry R. Beller – HRBeller@lbl.gov
Fuels Synthesis Division, Joint BioEnergy Institute

Aliphatic hydrocarbons are appealing targets for advanced cellulosic biofuels, as they are predominant components of petroleum-based gasoline and diesel fuels and thus would be compatible with existing engines and fuel distribution systems. We have studied alkene biosynthesis in Micrococcus luteus, a close relative of Sarcina lutea (now Kocuria rhizophila), which was previously reported to biosynthesize iso- and anteiso-branched, long-chain alkenes. The underlying biochemistry and genetics of alkene biosynthesis were not elucidated in those studies. We show here that heterologous expression of a threegene cluster from M. luteus (Mlut_13230-13250) in a fatty-acid overproducing E. coli strain resulted in production of long-chain alkenes, predominantly 27:3 and 29:3 (no. carbon atoms: no. C=C bonds). Heterologous expression of Mlut_13230 (oleA) alone produced no long-chain alkenes but unsaturated aliphatic monoketones, predominantly 27:2, and in vitro studies with the purified Mlut_13230 protein and tetradecanoyl-CoA produced the same C27 monoketone. Gas chromatography-time of flight mass spectrometry confirmed the elemental composition of all detected long-chain alkenes and monoketones (putative intermediates of alkene biosynthesis). Negative controls demonstrated that the M. luteus genes were responsible for production of these metabolites. Studies with wild-type M. luteus showed that the expression of Mlut 13230-13250 and 29:1 alkene biosynthesis both corresponded with bacterial population over time. We propose a metabolic pathway for alkene biosynthesis starting with acyl-CoA (or -ACP) thioesters and involving decarboxylative Claisen condensation as a key step, which we believe is catalyzed by OleA. Such activity is consistent with our data and with the homology of Mlut_13230 (OleA) to FabH (β-ketoacyl-ACP synthase III), which catalyzes decarboxylative Claisen condensation during fatty acid biosynthesis.

This work was part of the DOE Joint BioEnergy Institute (http://www.jbei.org) supported by the U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research, through contract DE-AC02-05CH11231 between Lawrence Berkeley National Laboratory and the U.S. Department of Energy.

